

Figure 1

A. Nucleic acid encoding human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:1)

1 TACTGGAAGGTGGCGTGCCCTCCTCTGGCTGGTACC**ATG**CAGCTCCCAC**T**
51 GGCCCTGTGTCTCGTCTGCCTGCTGGTACACACAGCC**T**CCGTGTAGTGG
101 AGGGCAGCGGGTGGCAGCGCTTCAAGAAATGATGCCACGGAAATCATCCCC
151 GAGCTCGGAGAGTACCCCGAGCCTCCACCGGAGCTGGAGAACACAGAC
201 CATGAACCGGCGGAGAACGGAGGGCGGCCTCCCCACCACCCCTTTGAGA
251 CCAAAAGCTGTCCGAGTGCAGCTGCGCGAGCTGCATTCACCCGCTAC
301 GTACCCGATGGGCGGTGCGCAGCGCAAGCGCGTACCAGGACTGGTGTG
351 CTCGGCCAGTGCGGCCCGGCGCGCTGCTGCCCAACGCCATCGGCCGCG
401 GCAAGTGGTGCGACACTAGTGGGCCCGACTTCCGCTGCATCCCCGACCG
451 TACCGCGCGCAGCGCTGCAGCTGCTGTCCCGGTGGTGAGGCGCCGCG
501 CGCGCGCAAGGTGCGCCTGGTGGCTCTGTGCAAGTGCAAGCGCCTCACCC
551 GCTTCCACAACCACTCGGAGCTCAAGGACTTCGGGACCGAGGCCGCTCGG
601 CCGCAGAAAGGCCGGAAGCCGCGGCCCGCGCCCGAGCGCCAAAGCCAA
651 CCAGGCGGAGCTGGAGAACGCCTAC**TAG**AGCCCGCCGCGCCCCCTCCCCA
701 CCGCGCGGCGCCCCGCGCCTGAACCCGCGCCCCACATTCTGTCTCTGCG
751 GCGTGGTTT

B. Human Cloaked-2 polypeptide most likely mature form (SEQ ID NO:2)

1 QGWQAFKNDAT E I I P E L G E Y P E P P P E L E N N K T M N R A E N G G R P P H P F E T K
51 D V S E Y S **C** R E L H F T R Y V T D G P **C** R S A K P V T E L V C S G Q C G P A R L L P N A I G R G K
101 W W R P S G P D F R **C** I P D R Y R A Q R V Q L L **C** P G G E A P R A R K V R L V A S C K C K R L T R F
151 H N Q S E L K D F G T E A A R P O K G R K P R P R A R S A K A N Q A E L E N A Y

C. Human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:5)

1 MQLPLALCLVCLLVHTAFRVVEGQGWQAFKNDATETIIPELGEYPEPPPEL
51 ENNKMTMNAENGGRPPHPHFETKDVSEYSCRELHFTRYVTDGPCRSAKPV
101 TELVCSGQCGLPARLLPNAIGRGKWWRPSPGPDFRCIPDRYRAQRVQLLCPG
151 GEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAARPQKGRKPRPRAR
201 SAKANOAELENAY

Figure 2

A. Nucleic acid encoding mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:3)

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1  ATGCAGCCCTCACTAGCCCCGTGCCTCATCTGCCTACTTGTGCACGCTGC
51  CTTCTGTGCTGTGGAGGGCCAGGGGTGGCAAGCCTTCAGGAATGATGCCA
101 CAGAGGTCACTCCAGGGCTTGGAGAGTACCCCGAGCCTCCTCCTGAGAAC
151 AACCAGACCATGAACCGGGCGGAGAAATGGAGGCAGACCTCCCCACCATCC
201 CTATGACGCCAAAGATGTGTCCGAGTACAGCTGCCGCGAGCTGCACTACA
251 CCCGCTTCCTGACAGACGGCCCATGCCGCAGCGCCAAGCCGGTCACCGAG
301 TTGGTGTGCTCCGGCCAGTGGCGCCCCCGCGCGGCTGCTGCCCAACGCCAT
351 CGGGCGCGTGAAGTGGTGGCGCCCCGAACGGACCGGATTCCGCTGCATCC
401 CGGATCGCTACCGCGCGCAGCGGGTGCAGCTGCTGTGCCCCGGGGGCGCG
451 GCGCCGCGCTCGCGCAAGGTGCGTCTGGTGGCCTCGTGCAAGTGCAAGCG
501 CCTACCCGCTTCACAAACAGTCGGAGCTCAAGGACTTCGGGCCGGAGA
551 CCGCGCGGCGCAGAAGGGTCGCAAGCCGCGGCCCGCGCCCGGGGAGCC
601 AAAGCCAACCAGGCGGAGCTGGAGAACGCCTACTAG

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B. Mouse Cloaked-2 polypeptide most likely mature form (SEQ ID NO:4)

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1  QGWQAFRNDATEVIPGLGEYPEPPPENQTMNRAENGGRPPHHHPYDAKDV
51  SEYSCRELHYTRFLTDGPCRSAPVTELVCSGQCGPARLLPNAIGRVKWW
101 RPNGPDFRCIPDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRFHN
151 QSELKDFGPETARPQKGRKPRPGARGAKANQAELENAY

```

C. Mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:6)

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1  MQPSLAPCLICLLVHAAFCAVEGQGWQAFRNDATEVIPGLGEYPEPPPEN
51  NQTMNRAENGGRPPHHHPYDAKDVSEYSCRELHYTRFLTDGPCRSAPVTE
101 LVCSGQCGPARLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLLCPGGA
151 APRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPGARGA
201 KANQAELENAY

```

Figure 3

GAP of: Human Cloaked-2 check: 5775 from: 1 to: 213
 to: Mouse Cloaked-2 check: 9489 from: 1 to: 211

Symbol comparison table:
 /GCGDISK/gcg10/gcgcore/data/rundata/blosum62.cmp
 CompCheck: 6430

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	1028	Length:	213
Ratio:	4.872	Gaps:	1
Percent Similarity:	91.469	Percent Identity:	88.152

Match display thresholds for the alignment(s):

| = IDENTITY
 : = 2
 . = 1

Human Cloaked-2 (SEQ ID NO: 5) x
Mouse Cloaked-2 (SEQ ID NO: 6)

```

1 MQLPLALCLVCLLVHTAFRVVEGQGWQAFKNDATETIIPELGEYPEPPPEL 50
  ||  ||  ||  |:|||||  ||  |||||||||:|||||:|  |||||||||
1 MQPSLAPCLICLLVHAAFCAVEGQGWQAFRNDATTEVIPGLGEYPEPPP.. 48

51 ENNKTMNRAENGGRPPHHPFETKDVSEYSCRELHFTRYVTDGPCRSAKPV 100
  |||.|||||||||||||||:|:|  |||||||||||:|:|.|||||||||
49 ENNQTMNRAENGGRPPHHPYDAKDVSEYSCRELHYTRFLTDGPCRSAKPV 98

101 TELVCSGQCGPARLLPNAIGRGKWWRPSPGPDFRCIPDRYRAQRVQLLCPG 150
  |||||||||||||||||||  |||.|||||||||
99 TELVCSGQCGPARLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLLCPG 148

151 GEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAARPQKGRKPRPRAR 200
  | |||.|||||||||||||||||  |||||||||||
149 GAAPRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPGAR 198

201 SAKANQAELENAY 213
  |||||||||||
199 GAKANQAELENAY 211
  
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Figure 3 = 44360

Figure 4

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GAP of: Human Cloaked-1 check: 1888 from: 1 to: 183
      to: Human Cloaked-2 check: 185 from: 1 to: 190
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```
Symbol comparison table:
/GCGDISK/gcgl0/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
```

```

      Gap Weight:      8      Average Match:   2.912
    Length Weight:      2      Average Mismatch: -2.003

      Quality:       335      Length:       196
      Ratio:    1.831      Gaps:           6
Percent Similarity: 52.542  Percent Identity: 42.938

```

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Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1
```

$$\frac{\text{Human Cloaked-1 (SEQ ID NO: 25)}}{\text{Human Cloaked-2 (SEQ ID NO: 2)}}$$

```

1 .....FKNDATEILYSHVVKP.VPAHPSSNSTLNQARNGGRHFSNTGLDR 44  

    |||||:: | :| :||| :  

1 QGWQAFKNDATEIIPELGEYPEPPPELENNKTMNRAENGGRP.PHHPFET 49  

     .  

45 NTRVQVGCRELRSTKYISDGQCTSISPLKELVCAGECLPLPVLPNWIGGG 94  

    : |||| |:|.|| | | . ||||.:| | .||| |||  

50 KDVSEYSCRELHFTRYVTDGPCRSAKPVTELVCGSQCGPARLLPNAIGRG 99  

     .  

95 YGTKYWSRRSSQEWRCVNDKTRTQR IQLQCQDG.STRTYKITVV TACKCK 143  

    |:| | :.||: | :| :|| | | . | |: .| .||||  

100 ...KWW.RPSGPDFRCIPDRYAQRVQLLCPGGEAPRARKVRLVASCKCK 145  

     .  

144 RYTROHNESHNFESMSPAKPVQHHRERKRASKSSKHMS..... 183  

    | || ::| :| : | || :|. .  

146 RLTRPHNQSELKDGFTEAARPQKGRKPRPRA.RSAKANQAELNAY 190

```